

What is claimed is:

1. A method for determining whether a human immunodeficiency virus type 1 (HIV-1) has an increased likelihood of having a reduced susceptibility to treatment with a protease inhibitor, comprising: detecting whether the protease encoded by said HIV-1 exhibits the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at amino acid position 11, 32, 33, 34, 43, 46, 47, 48, 50, 54, 58, 71, 76, 79, 82, 83, 84, 91 or 95 of an amino acid sequence of said protease, wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having reduced susceptibility to treatment with the protease inhibitor, with the proviso that said mutation is not V32I, M46I, M46L, I47V, I50V, I54L, I54M or I84V.
2. The method of claim 1, wherein said protease inhibitor is amprenavir.
3. A method of determining whether an individual infected with HIV-1 has an increased likelihood of having a reduced susceptibility to treatment with a protease inhibitor, comprising: detecting, in a sample from said individual, the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at amino acid position 11, 32, 33, 34, 43, 46, 47, 48, 50, 54, 58, 71, 76, 79, 82, 83, 84, 91 or 95 of the amino acid sequence of the protease of the HIV, wherein the presence of said mutation indicates that the individual has an increased likelihood of having reduced susceptibility to treatment with the protease inhibitor, with the proviso that said mutation is not V32I, M46I, M46L, I47V, I50V, I54L, I54M or I84V.
4. The method of claim 3, wherein said protease inhibitor is amprenavir.
5. The method of claim 3, wherein the individual is undergoing or has undergone prior treatment with an anti-viral drug.
6. An isolated oligonucleotide between about 10 and about 40 nucleotides long encoding a portion of a HIV protease in a HIV that comprises at least one mutation at amino acid position 11, 32, 33, 34, 43, 46, 47, 48, 50, 54, 58, 71, 76, 79, 82, 83, 84, 91 or 95 of an amino acid sequence of said protease in said human immunodeficiency virus,

wherein the mutation is associated with reduced susceptibility to a protease inhibitor, with the proviso that said mutation is not V32I, M46I, M46L, I47V, I50V, I54L, I54M or I84V.

7. A method for determining whether a HIV-1 has an increased likelihood of having reduced susceptibility to treatment with a protease inhibitor, comprising:
detecting whether the protease encoded by said HIV-1 exhibits the presence or absence of one or more HIV-1 protease mutations listed in Table 1; and
applying a set of rules to said mutations as provided in Table 4,
wherein said HIV-1 has an increased likelihood of being resistant to treatment with said protease inhibitor if said set of rules is satisfied.
8. The method of claim 7, wherein said protease inhibitor is amprenavir.
9. A method for determining whether an individual infected with a HIV-1 has an increased likelihood of having reduced susceptibility to treatment with a protease inhibitor, comprising:
detecting, in a sample from said individual, the presence or absence of one or more HIV protease mutations listed in Table 1; and
applying a set of rules to said mutations as provided in Table 4,
wherein said individual has an increased likelihood of being resistant to treatment with said protease inhibitor if said set of rules is satisfied.
10. The method of claim 9, wherein said protease inhibitor is amprenavir.
11. The method of claim 9, wherein the individual is undergoing or has undergone prior treatment with an anti-viral drug.
12. The method of claim 1, wherein the amino acid at position 11, 33, 43, 48, 54, 71, 76, 82, 84, 91 or 95 of said protease is an amino acid having a neutral, hydrophobic or non-polar side chain.
13. The method of claim 12, wherein the amino acid at position 11 of said protease is I or L.

14. The method of claim 12, wherein the amino acid at position 33 of said protease is F.
15. The method of claim 1, wherein the amino acid at position 34 of said protease is an amino acid having a neutral, polar or hydrophilic side chain.
16. The method of claim 15, wherein the amino acid at position 34 of said protease is Q.
17. The method of claim 12, wherein the amino acid at position 43 of said protease is T.
18. The method of claim 12, wherein the amino acid at position 48 of said protease is M.
19. The method of claim 12, wherein the amino acid at position 54 of said protease is A.
20. The method of claim 12, wherein the amino acid at position 71 of said protease is L.
21. The method of claim 12, wherein the amino acid at position 76 of said protease is V.
22. The method of claim 12, wherein the amino acid at position 82 of said protease is A or F.
23. The method of claim 12, wherein the amino acid at position 84 of said protease is A.
24. The method of claim 12, wherein the amino acid at position 91 of said protease is A or V.
25. The method of claim 12, wherein the amino acid at position 95 of said protease is F.
26. The method of claim 1, wherein the amino acid at position 54 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.
27. The method of claim 1, wherein the amino acid at position 54 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.
28. The method of claim 27, wherein the amino acid at position 54 of said protease is S or T.

29. The method of claim 1, wherein the amino acid at position 58 or 83 of said protease is an amino acid with an acidic, hydrophilic or polar side chain.
30. The method of claim 29, wherein the amino acid at position 58 of said protease is E.
31. The method of claim 1, wherein the amino acid at position 83 of said protease is D.
32. The method of claim 1, wherein the amino acid at position 79 of said protease is an amino acid with a neutral, hydrophobic, non-polar, acidic, hydrophilic or polar side chain.
33. The method of claim 1, wherein the amino acid at position 79 of said protease is an amino acid with a neutral, hydrophobic or non-polar side chain.
34. The method of claim 1, wherein the amino acid at position 79 of said protease is an amino acid with an acidic, neutral, hydrophilic or polar side chain.
35. The method of claim 1, wherein the amino acid at position 79 of said protease is any amino acid, with the proviso that it is not P.
36. The method of claim 1, wherein the amino acid at position 84 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.
37. The method of claim 1, wherein the amino acid at position 84 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.
38. The method of claim 38, wherein the amino acid at position 84 of said protease is C.
39. The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.
40. The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.
41. The method of claim 40, wherein the amino acid at position 91 of said protease is S.

42. The method of claim 1, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 of the amino acid positions.